Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:20:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716980.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR9716980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716980.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:20:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,397,306
Mapped reads	4,634,018 / 85.86%
Unmapped reads	763,288 / 14.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,253 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	224,656 / 4.16%
Duplication rate	3.43%
Clipped reads	4,644,746 / 86.06%

2.2. ACGT Content

Number/percentage of A's	61,368,899 / 23.58%
Number/percentage of C's	50,680,261 / 19.48%
Number/percentage of T's	81,320,375 / 31.25%
Number/percentage of G's	66,830,077 / 25.68%
Number/percentage of N's	3,814 / 0%
GC Percentage	45.16%

2.3. Coverage

Mean	0.0841

Standard Deviation	0.6106

2.4. Mapping Quality

Mean Mapping Quality	41.49

2.5. Mismatches and indels

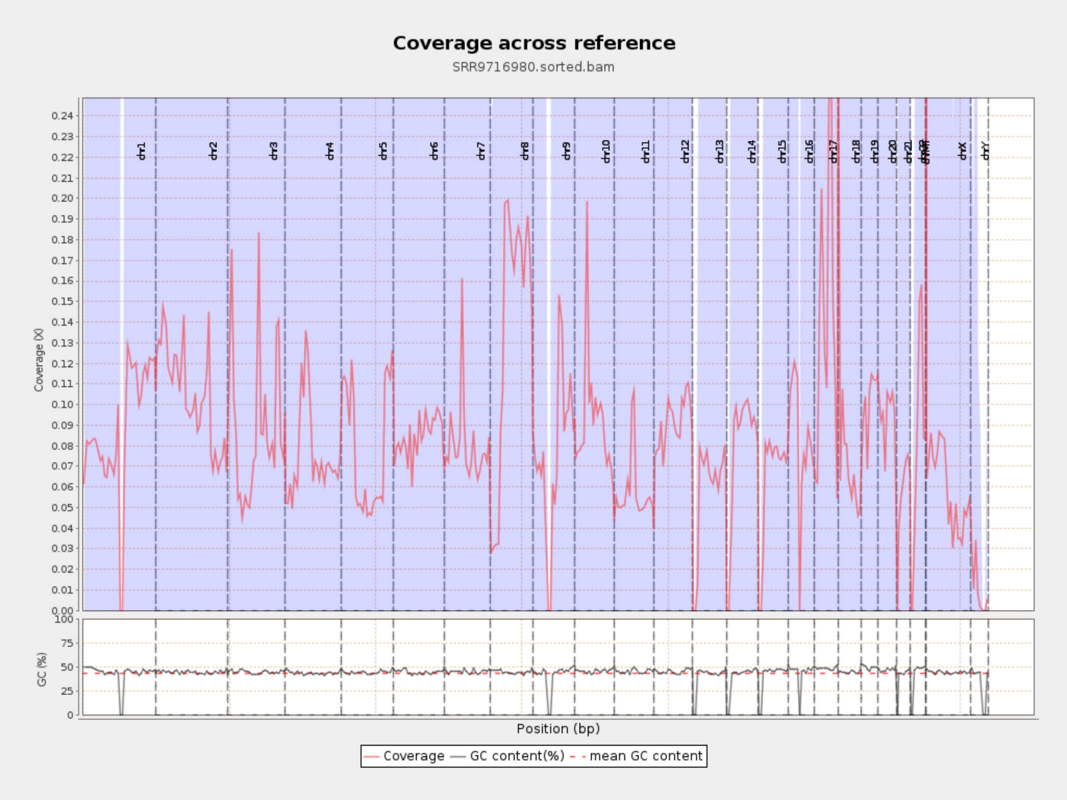
General error rate	0.53%
Mismatches	1,347,137
Insertions	16,993
Mapped reads with at least one insertion	0.36%
Deletions	47,019
Mapped reads with at least one deletion	1.01%
Homopolymer indels	40.99%

2.6. Chromosome stats

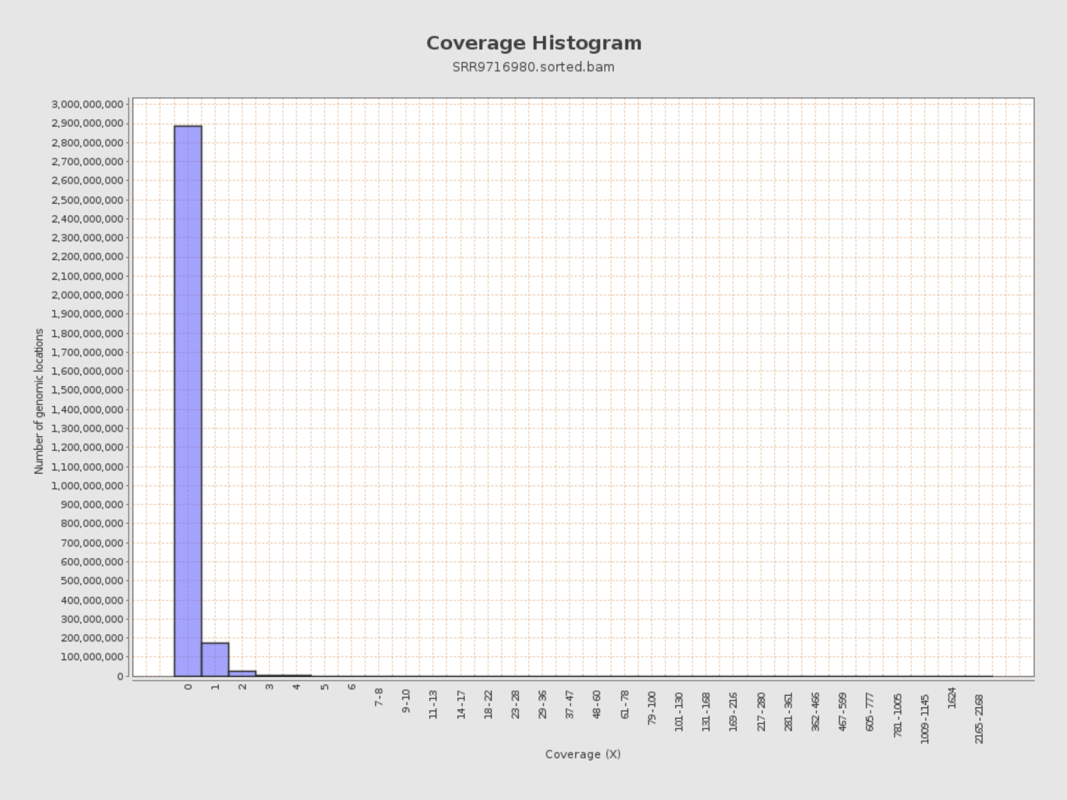
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21955501	0.0881	0.817
chr2	243199373	25567339	0.1051	0.9996
chr3	198022430	17341821	0.0876	0.3831
chr4	191154276	14573942	0.0762	0.3899
chr5	180915260	14263852	0.0788	0.3436
chr6	171115067	14466016	0.0845	0.4447
chr7	159138663	12873450	0.0809	1.2482

chr8	146364022	20227715	0.1382	0.59
chr9	141213431	10646278	0.0754	0.4401
chr10	135534747	12462265	0.0919	0.7152
chr11	135006516	7871773	0.0583	0.4277
chr12	133851895	12303715	0.0919	0.3796
chr13	115169878	6739515	0.0585	0.2964
chr14	107349540	8529069	0.0795	0.368
chr15	102531392	6402111	0.0624	0.322
chr16	90354753	7418761	0.0821	0.3871
chr17	81195210	11873154	0.1462	0.5268
chr18	78077248	6082307	0.0779	0.7251
chr19	59128983	5933625	0.1004	0.7157
chr20	63025520	5969607	0.0947	0.3864
chr21	48129895	2705913	0.0562	0.3225
chr22	51304566	4170432	0.0813	0.3611
chrMT	16571	54750	3.304	2.7786
chrX	155270560	9213220	0.0593	0.3808
chrY	59373566	632961	0.0107	0.2543

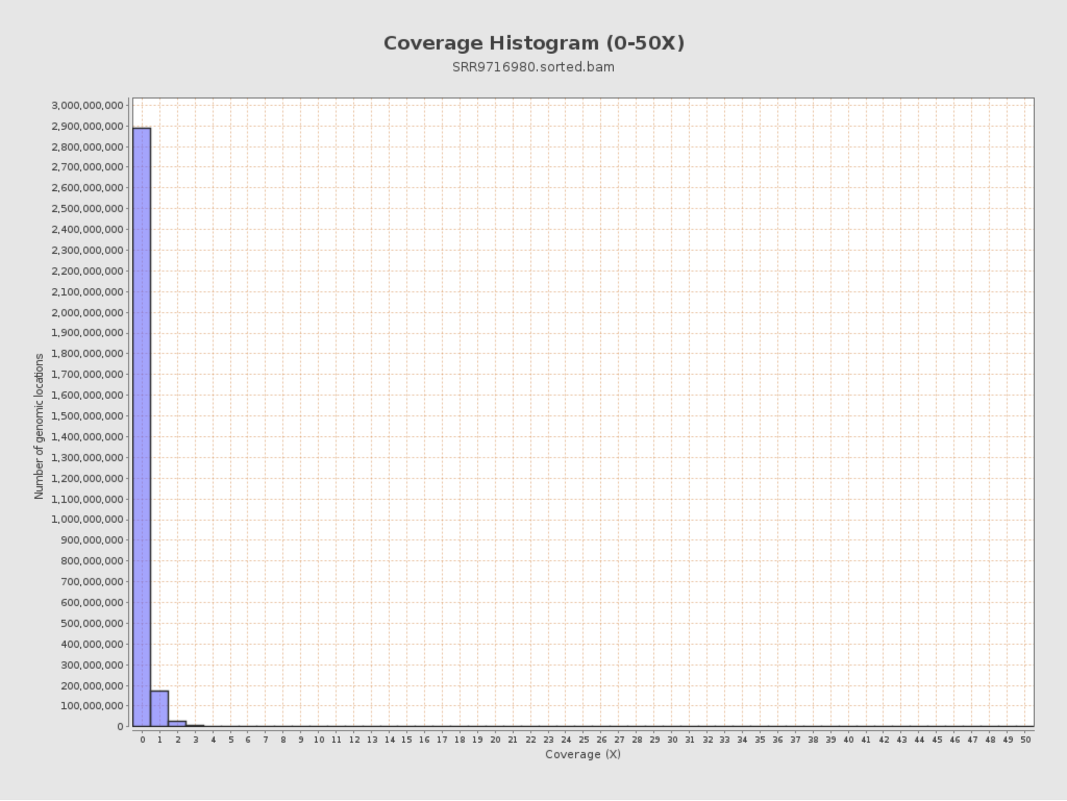
3. Results : Coverage across reference



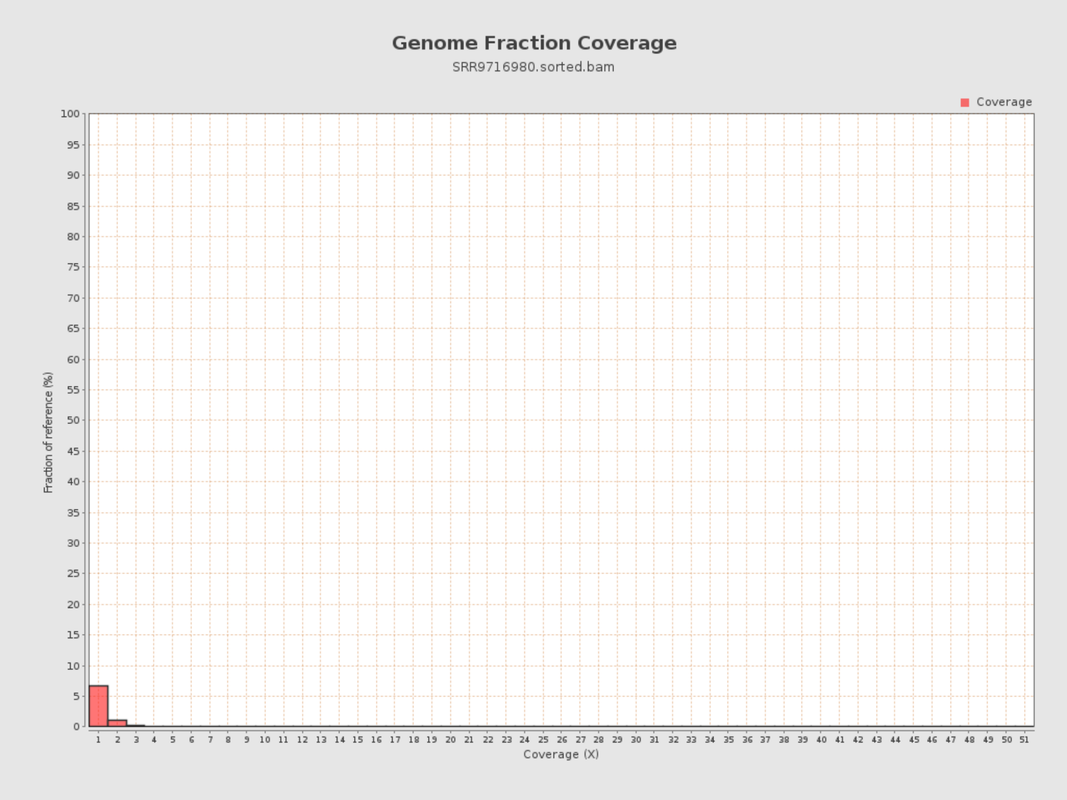
4. Results : Coverage Histogram



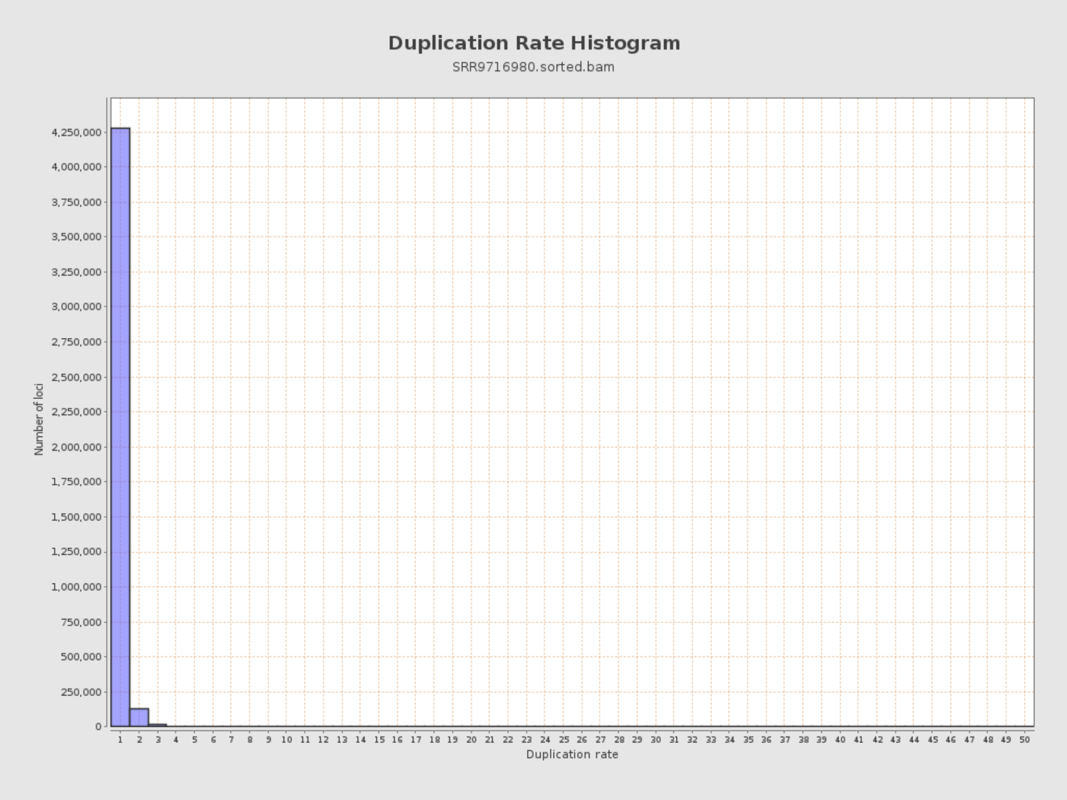
5. Results : Coverage Histogram (0-50X)



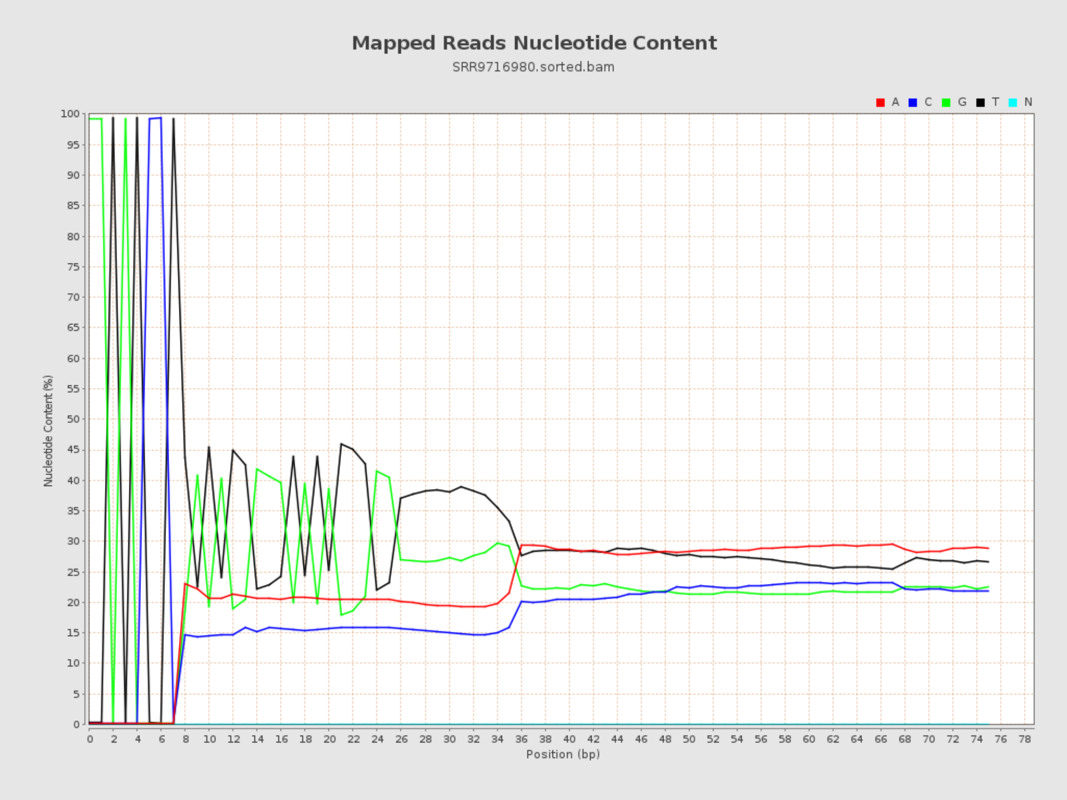
6. Results : Genome Fraction Coverage



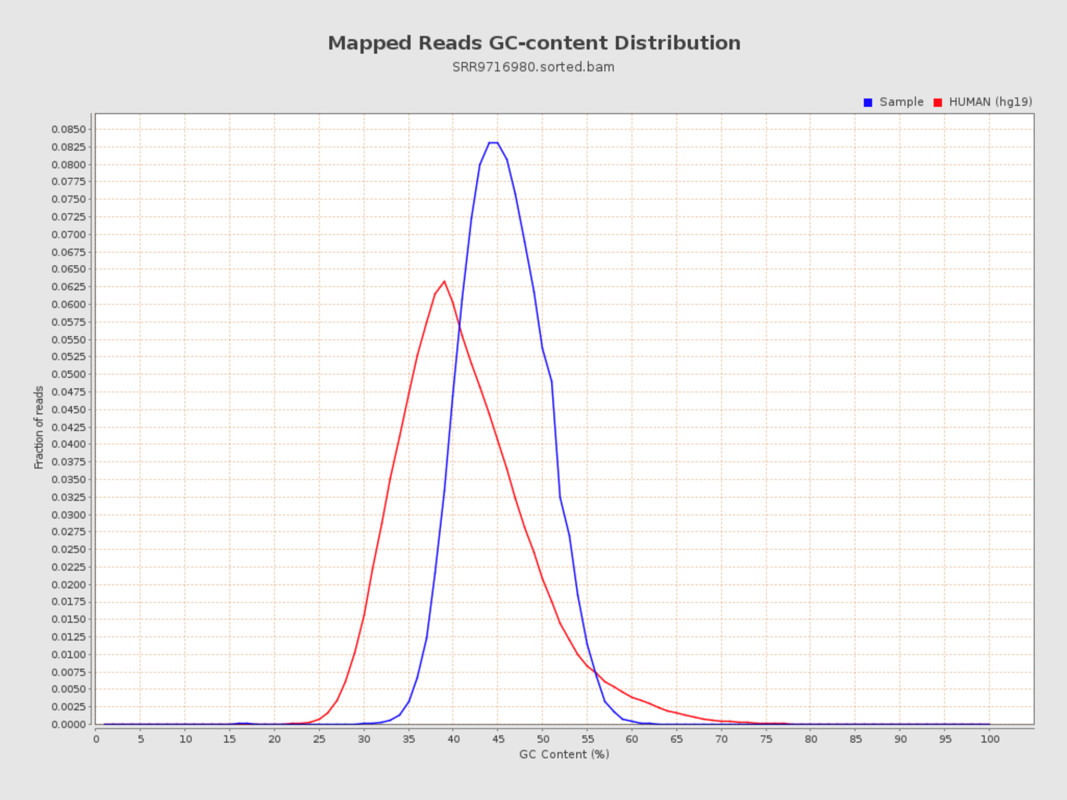
7. Results : Duplication Rate Histogram



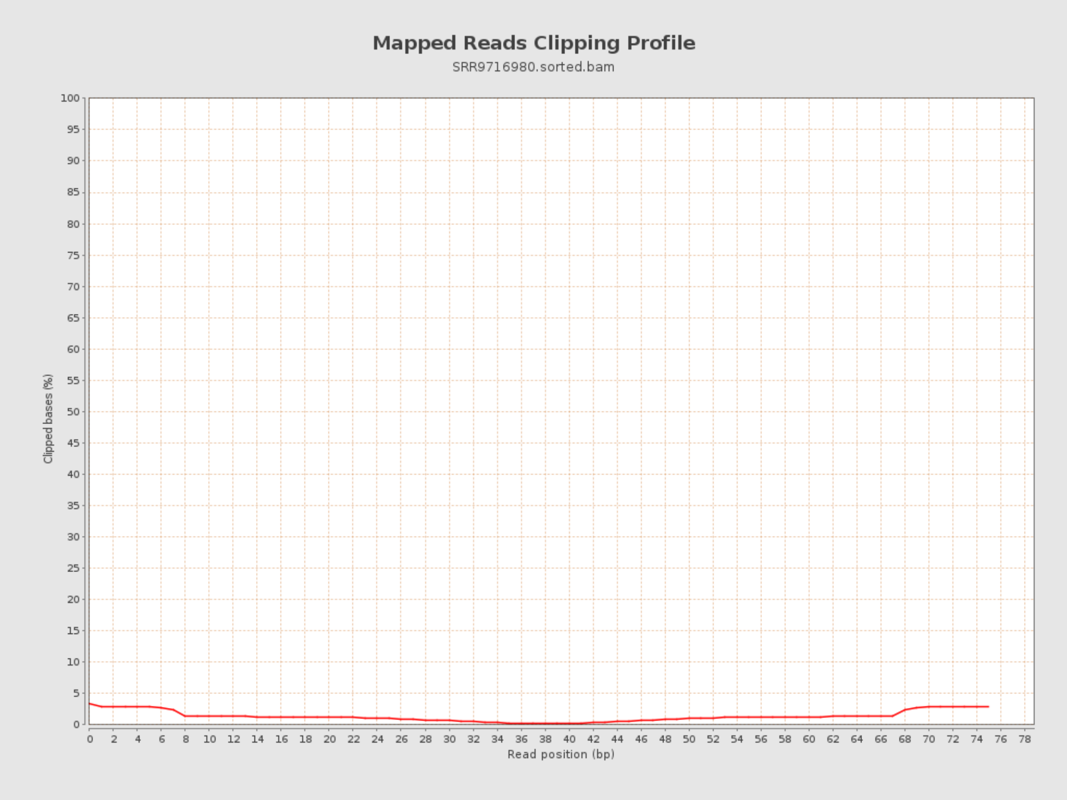
8. Results : Mapped Reads Nucleotide Content



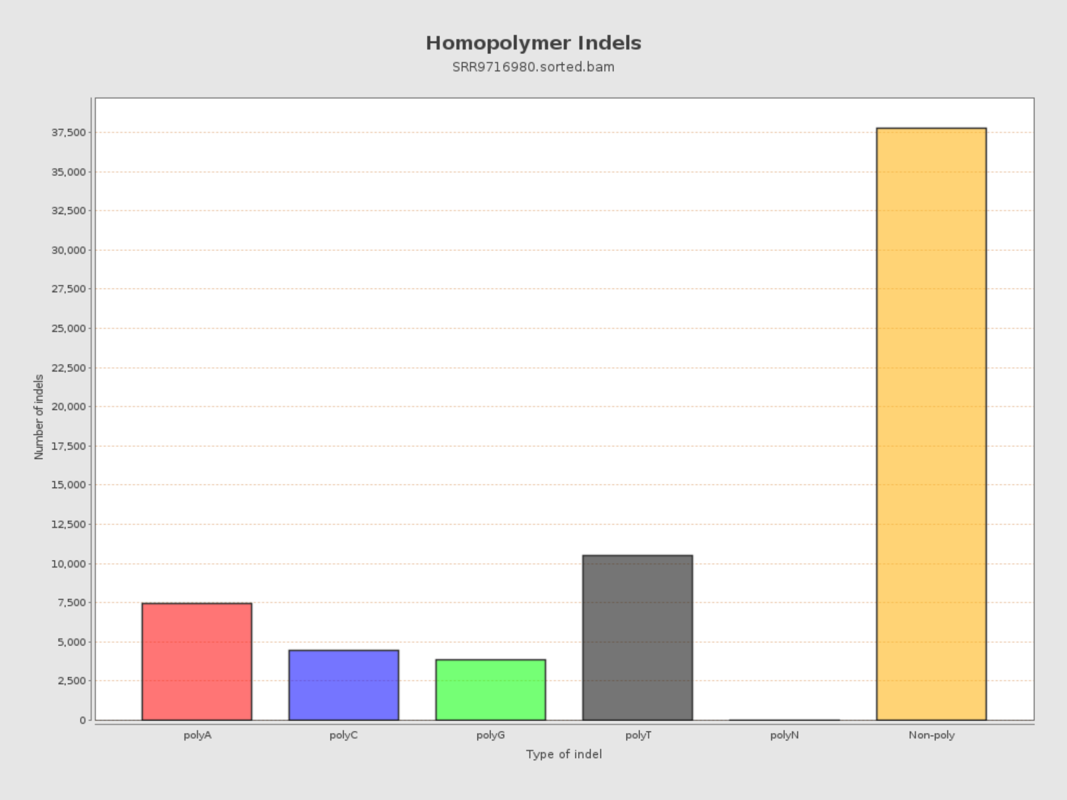
9. Results : Mapped Reads GC-content Distribution



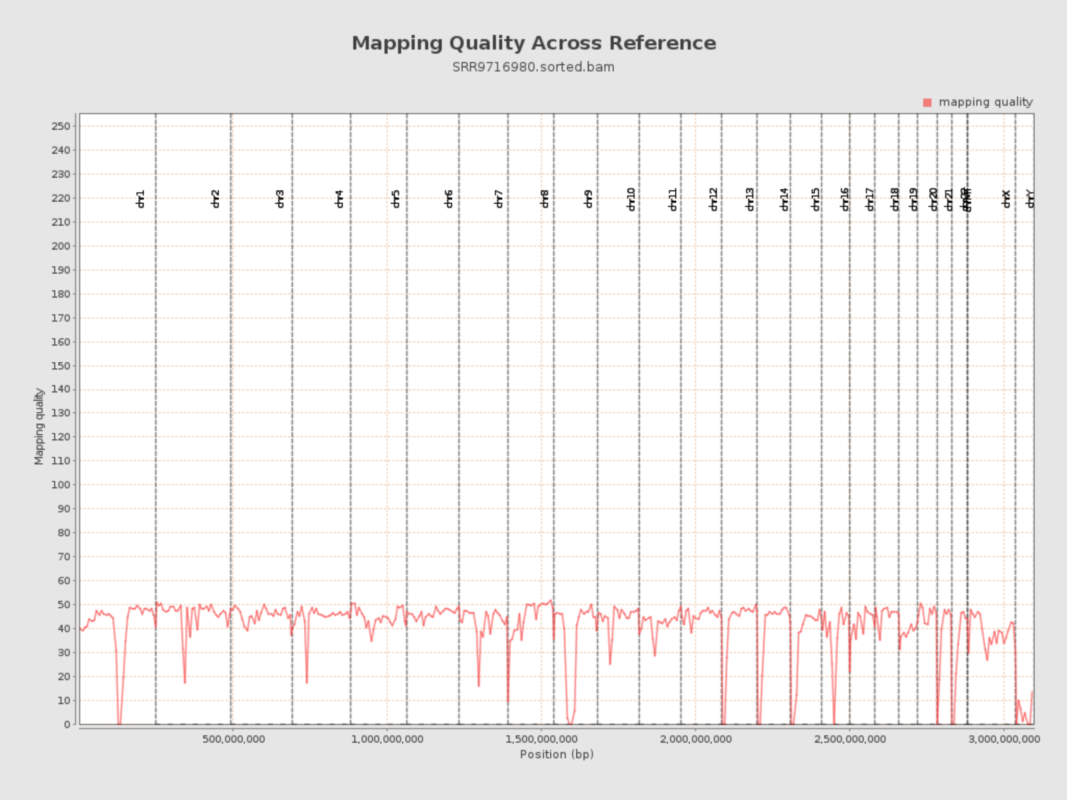
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram